EXHIBIT A

Bone morphogenetic protein 2 precursor - Homo sapiens (Human) - Microsoft Internet Explorer

파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)

뒤로 검색 즐겨찾기 클립북

주소(D) http://www.uniprot.org/uniprot/P12643

Sequences

	Sequence		Length	Mass (Da)	Tools
☐	P12643-1 [UniParc].	FASTA	396	44,702	Blast go

Last modified October 1, 1989. Version 1.
Checksum: 20653A3987B25E60

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        10         20         30         40         50         60
MVAGTRCLLA LLLPQVLLGG AAGLVPELGR RKFAAASSGR PSSQPSDEVL SEFELRLLSM

        70         80         90        100        110        120
FGLKQRPTPS RDAVVPPYML DLYRRHSGQP GSPAPDHRLE RAASRANTVR SFHHEESLEE

       130        140        150        160        170        180
LPETSGKTTR RFFFNLSSIP TEEFITSAEL QVFREQMQDA LGNNSSFHHR INIYEIIKPA

       190        200        210        220        230        240
TANSKFPVTR LLDTRLVNQN ASRWESFDVT PAVMRWTAQG HANHGFVVEV AHLEEKQGVS

       250        260        270        280        290        300
KRHVRISRSL HQDEHSWSQI RPLLVTFGHD GKGHPLHKRE KRQAKHKQRK RLKSSCKRHP

       310        320        330        340        350        360
LYVDFSDVGW NDWIVAPPGY HAFYCHGECP FPLADHLNST NHAIVQTLVN SVNSKIPKAC

       370        380        390
CVPTELSAIS MLYLDENEKV VLKNYQDMVV EGCGCR
```

→BMP-2 sequence (283~396)
→1~282 : Signal peptide + Propeptide

→SEQ ID No:3 of the present invention: 2-18 of the above BMP-2 (red underline) : 17 amino acids

→SEQ ID No:6 of the present invention: 24-40 of the above BMP-2(pink underline) : 17 amino acids

•SEQ ID No: 10 of the present invention: 283-302 of BMP- 2 precusor (violet underline)
• SEQ ID No: 11 of the present invention: **355-374** of BMP-2 precusor (green underline)

• SEQ ID No: 12 of the present invention: 370-390 of BMP-2 precusor (yellow underline)

Bone morphogenetic protein 2 precursor - Homo sapiens (Human) - Microsoft Internet Explorer

파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)

뒤로 검색 즐겨찾기

주소(D) http://www.uniprot.org/uniprot/P12643

Sequence annotation (Features)

	Feature key	Position(s)	Length	Description	Graphical view	Feature identifier
Molecule processing						
☐	Signal peptide	1 – 23	23	Potential		
☐	Propeptide	24 – 282	259			PRO_0000033824
☐	Chain	283 – 396	114	Bone morphogenetic protein 2		PRO_0000033825
Amino acid modifications						
☐	Glycosylation	135	1	N-linked (GlcNAc...) Potential		
☐	Glycosylation	163	1	N-linked (GlcNAc...) Potential		
☐	Glycosylation	164	1	N-linked (GlcNAc...) Potential		
☐	Glycosylation	200	1	N-linked (GlcNAc...) Potential		
☐	Disulfide bond	296 ↔ 361				
☐	Disulfide bond	325 ↔ 393				
☐	Disulfide bond	329 ↔ 395				
☐	Disulfide bond	360		Interchain		

EXHIBIT B

Last modified October 1, 1989. Version 1.
Checksum: 79B01179DBB98204

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        10         20         30         40         50         60
MIPGNRMLMV VLLCQVLLGG ASHASLIPET GKKKVAEIQG HAGGRRSGQS HELLRDFEAT

        70         80         90        100        110        120
LLQMFGLRRR PQPSKSAVIP DYMRDLYRLQ SGEEEEEQIH STGLEYPERP ASRANTVRSF

       130        140        150        160        170        180
HHEEHLENIP GTSENSAFRF LFNLSSIPEN EVISSAELRL FREQVDQGPD WERGFHRINI

       190        200        210        220        230        240
YEVMKPPAEV VPGHLITRLL DTRLVHHNVT RWETFDVSPA VLRWTREKQP NYGLAIEVTH

       250        260        270        280        290        300
LHQTRTHQGQ HVRISRSLPQ GSGNWAQLRP LLVTFGHDGR GHALTRRRRA KRSPKHHSQR

       310        320        330        340        350        360
ARKKNKNCRR HSLYVDFSDV GWNDWIVAPP GYQAFYCHGD CPFPLADHLN STNHAIVQTL

       370        380        390        400
VNSVNSSIPK ACCVPTELSA ISMLYLDEYD KVVLKNYQEM VVEGCGCR
```

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→BMP-4 sequence (293~408).
→1~292 : Signal peptide + Propeptide

→ SEQ ID No: 4 of the present invention : 2-18 of the above BMP-4 (red underline) : 17 amino acids

•SEQ ID No: 14 of the present invention: 293-313 of BMP- 4 precusor (violet underline)

• SEQ ID No: 15 of the present invention : **366-386** of BMP-4 precusor (green underline)

• SEQ ID No: 16 of the present invention: 382-402 of BMP-4 precusor (yellow underline)

References

« Hide 'large scale' references

Sequence annotation (Features)

	Feature key	Position(s)	Length	Description	Graphical view	F
Molecule processing						
☐	Signal peptide	1 – 19	19	Potential		
☐	Propeptide	20 – 292	273			F
☐	Chain	293 – 408	116	Bone morphogenetic protein 4		F
Amino acid modifications						
☐	Glycosylation	143	1	N-linked (GlcNAc...) Potential		
☐	Glycosylation	208	1	N-linked (GlcNAc...) Potential		
☐	Glycosylation	350	1	N-linked (GlcNAc...) Potential		
☐	Glycosylation	365	1	N-linked (GlcNAc...) Potential		
☐	Disulfide bond	308 ↔ 373		By similarity		
☐	Disulfide bond	337 ↔ 405		By similarity		
☐	Disulfide bond	341 ↔ 407		By similarity		
☐	Disulfide bond	372		Interchain By similarity		

Distance

EXHIBIT C

Bone morphogenetic protein 6 precursor - Homo sapiens (Human) - Microsoft Internet Explorer

파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)

뒤로 검색 즐겨찾기 클립북

주소(D) http://www.uniprot.org/uniprot/P22004

Sequences

	Sequence		Length	Mass (Da)	Tools
☐	P22004-1 [UniParc].	FASTA	513	57,226	Blast go

Last modified August 1, 1991. Version 1.
Checksum: 3F19155B36049278

```
        10         20         30         40         50         60
MPGLGRRAQW LCWWWGLLCS CCGPPPLRPP LPAAAAAAAG GQLLGDGGSP GRTEQPPPSP

        70         80         90        100        110        120
QSSSGFLYRR LKTQEKREMQ KEILSVLGLP HRPRPLHGLQ QPQPPALRQQ EEQQQQQQLP

       130        140        150        160        170        180
RGEPPPGRLK SAPLFMLDLY NALSADNDED GASEGERQQS WPHEAASSSQ RRQPPPGAAH

       190        200        210        220        230        240
PLNRKSLLAP GSGSGGASPL TSAQDSAFLN DADMVMSFVN LVEYDKEFSP RQRHHKEFKF

       250        260        270        280        290        300
NLSQIPEGEV VTAAEFRIYK DCVMGSFKNQ TFLISIYQVL QEHQHRDSDL FLLDTRVVWA

       310        320        330        340        350        360
SEEGWLEFDI TATSNLWVVT PQHNMGLQLS VVTRDGVHVH PRAAGLVGRD GPYDKQPFMV

       370        380        390        400        410        420
AFFKVSEVHV RTTRSASSRR RQQSRNRSTQ SQDVARVSSA SDYNSSELKT ACRKHELYVS

       430        440        450        460        470        480
FQDLGWQDWI IAPKGYAANY CDGECSFPLN AHMNATNHAI VQTLVHLMNP EYVPKPCCAP

       490        500        510
TKLNAISVLY FDDNSNVILK KYRNMVVRAC GCH
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→BMP-6 sequence (375~513)
→ 1~374: Signal peptide + Propeptide

→ SEQ ID No: 5 of the present invention: 2-18 of the above BMP-6 (red underline) : 17 amino acids

•SEQ ID No: 18 of the present invention: 397-418 of BMP- 6 precusor (violet underline)

• SEQ ID No: 19 of the present invention: 472-490 of BMP-6 precusor (green underline)

• SEQ ID No: 20 of the present invention: 487-510 of BMP-6 precusor (yellow underline)

References

Bone morphogenetic protein 6 precursor – Homo sapiens (Human) – Microsoft Internet Explorer

파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)

뒤로 검색 즐겨찾기

주소(D) http://www.uniprot.org/uniprot/P22004

Sequence annotation (Features)

	Feature key	Position(s)	Length	Description	Graphical view
Molecule processing					
☐	Signal peptide	1 – 20	20	Potential	
☐	Propeptide	21 – 374	354	Potential	
☐	Chain	375 – 513	139	Bone morphogenetic protein 6	
Amino acid modifications					
☐	Glycosylation	241	1	N-linked (GlcNAc...) Potential	
☐	Glycosylation	269	1	N-linked (GlcNAc...) Potential	
☐	Glycosylation	386	1	N-linked (GlcNAc...) Potential	
☐	Glycosylation	404	1	N-linked (GlcNAc...) Potential	
☐	Glycosylation	454	1	N-linked (GlcNAc...) Potential	
☐	Disulfide bond	412 ↔ 478		By similarity	
☐	Disulfide bond	441 ↔ 510		By similarity	
☐	Disulfide bond	445 ↔ 512		By similarity	
☐	Disulfide bond	477		Interchain By similarity	
Natural variations					
☐	Natural variant	257	1	R → C: dbSNP rs10458105.	

EXHIBIT D

Bone morphogenetic protein 7 precursor - Homo sapiens (Human) - Microsoft Internet Explorer

파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)

뒤로 검색 즐겨찾기

주소(D) http://www.uniprot.org/uniprot/P18075&format=html

Details...

Sequences

	Sequence		Length	Mass (Da)	Tools
☐	P18075-1 [UniParc].	FASTA	431	49,313	Blast go

Last modified November 1, 1990. Version 1.
Checksum: 47AD5E45C6815F8A

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        10         20         30         40         50         60
MHVRSLRAAA PHSFVALWAP LFLLRSALAD FSLDNEVHSS FIHRRLRSQE RREMQREILS

        70         80         90        100        110        120
ILGLPHRPRP HLQGKHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS

       130        140        150        160        170        180
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHREFRFDL SKIPEGEAVT AAEFRIYKDY

       190        200        210        220        230        240
IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVFDITA TSNHWVVNPR

       250        260        270        280        290        300
HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS

       310        320        330        340        350        360
QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDWIIA PEGYAAYYCE

       370        380        390        400        410        420
GECAFPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY

       430
RNMVVRACGC H
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→BMP-7 sequence (293~431)
→ 1~292: Signal peptide + Propeptide

→ SEQ ID No: 21 of the present invention: 98-117 of BMP-7 (pink underline)
(The above sequence is equal to SEQ ID No: 23 of the present invention (390-409 of BMP-7 precusor.)

•SEQ ID No: 22 of the present invention: 320-340 of BMP-7 precusor (violet underline)

• SEQ ID No: 24 of the present invention: 405-423 of BMP-7 precusor (red underline)

Bone morphogenetic protein 7 precursor - Homo sapiens (Human) - Microsoft Internet Explorer

파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)

뒤로 검색 즐겨찾기

주소(D) http://www.uniprot.org/uniprot/P18075&format=html

Sequence annotation (Features)

	Feature key	Position(s)	Length	Description	Graphical view	Feature identifier
Molecule processing						
☐	Signal peptide	1 – 29	29	Potential		
☐	Propeptide	30 – 292	263	Ref.5		PRO_0000033876
☐	Chain	293 – 431	139	Bone morphogenetic protein 7		PRO_0000033877
Amino acid modifications						
☐	Glycosylation	187	1	N-linked (GlcNAc...) Potential		
☐	Glycosylation	302	1	N-linked (GlcNAc...) Potential		
☐	Glycosylation	321	1	N-linked (GlcNAc...) Potential		
☐	Glycosylation	372	1	N-linked (GlcNAc...) Potential		
☐	Disulfide bond	330 ↔ 396				
☐	Disulfide bond	359 ↔ 428				
☐	Disulfide bond	363 ↔ 430				
☐	Disulfide bond	395		Interchain		

Secondary structure

Helix Strand Turn

EXHIBIT E

Partial translation for KR 10-2004-0019010

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[Disclosure of invention]

<15> To achieve the above object, the present invention provides a barrier membrane and a implant which have a cell adhesion-inducing peptide and/or tissue growth factor-derived peptide immobilized on the surface of the membrane or the implant bonded with a cross-linking agent.

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<19> Specifically, the cell adhesion-inducing peptide is preferably a peptide having an amino acid sequence of SED ID NO: 1. More preferably, it is an amino acid sequence of SEQ ID NO: 2 or an amino acid sequence of SEQ ID NO: 3 designed to maintain the structural stability of the amino acid sequence of SEQ ID NO: 1, RGD. Furthermore, the tissue growth factor-derived peptide is a peptide identified and chemically synthesized from the active site of the tissue growth factor. Preferably it is at least one peptide selected from the group consisting of the following peptides:

<20> (a) the amino acid sequence at positions 283-302 (SEQ ID NO: 4), the amino acid sequence at positions 335-353 (SEQ ID NO: 5) and the amino acid sequence at positions 370-390 (SEQ ID NO: 6) of bone morphogenetic proteins (BMP)-2;

<21> the amino acid sequence at positions 293-313 (SEQ ID NO: 7), the amino acid sequence at positions 360-379 (SEQ ID NO: 8) and the amino acid sequence at positions 382-402 (SEQ ID NO: 9) of BMP-4;

<22> the amino acid sequence at positions 397-418 (SEQ ID NO: 10), the amino

acid sequence at positions 472-490 (SEQ ID NO: 11) and the amino acid sequence at positions 487-510 (SEQ ID NO: 12) of BMP-6;

<23> the amino acid sequence at positions 320-340 (SEQ ID NO: 13), the amino acid sequence at positions 390-409 (SEQ ID NO: 14) and the amino acid sequence at positions 405-423 (SEQ ID NO: 15) of BMP-7;

<24> (b) the amino acid sequence at positions 199-204 (SEQ ID NO: 16), the amino acid sequence at positions 151-158 (SEQ ID NO: 17), the amino acid sequence at positions 275-291 (SEQ ID NO: 18), the amino acid sequence at positions 20-28 (SEQ ID NO: 19), the amino acid sequence at positions 65-90 (SEQ ID NO: 20), the amino acid sequence at positions 150-170 (SEQ ID NO: 21) and the amino acid sequence at positions 280-290 (SEQ ID NO: 22) of bone sialoprotein,

<25> (c) the amino acid sequence at positions 242-250 (SEQ ID NO: 23), the amino acid sequence at positions 279-299 (SEQ ID NO: 24) and the amino acid sequence at positions 343-361 (SEQ ID NO: 25) of a transforming growth factor beta 1,

<26> (d) the amino acid sequence at positions 100-120 (SEQ ID NO: 26) and the amino acid sequence at positions 121-140 (SEQ ID NO: 27) of a platelet-derived growth factor,

<27> (e) the amino acid sequence at positions 23-31 (SEQ ID NO: 28) and the amino acid sequence at positions 97-105 (SEQ ID NO: 29) of an acidic fibroblast growth factor,

<28> (f) the amino acid sequence at positions 16-27 (SEQ ID NO: 30), the amino acid sequence at positions 37-42 (SEQ ID NO: 31), the amino acid sequence at positions

78-84 (SEQ ID NO: 32) and the amino acid sequence at positions 107-112 (SEQ ID NO: 33) of a basic fibroblast growth factor,

<29> (g) the amino acid sequence at positions 255-275 (SEQ ID NO: 34), the amino acid sequence at positions 475-494 (SEQ ID NO: 35) and the amino acid sequence at positions 551-573 (SEQ ID NO: 36) of dentin sialoprotein,

<30> (h) the amino acid sequence at positions 63-83 (SEQ ID NO: 37), the amino acid sequence at positions 84-103 (SEQ ID NO: 38), the amino acid sequence at positions 104-116 (SEQ ID NO: 39) and the amino acid sequence at positions 121-140 (SEQ ID NO: 40) of a heparin binding EGF-like growth factor,

<31> (i) the amino acid sequence at positions 326-350 (SEQ ID NO: 41), the amino acid sequence at positions 351-371 (SEQ ID NO: 42), the amino acid sequence at positions 372-400 (SEQ ID NO: 43), the amino acid sequence at positions 401-423 (SEQ ID NO: 44), the amino acid sequence at positions 434-545 (SEQ ID NO: 45), the amino acid sequence at positions 546-651 (SEQ ID NO: 46), the amino acid sequence at positions 1375-1433 (SEQ ID NO: 47), the amino acid sequence at positions 1435-1471 (SEQ ID NO: 48), the amino acid sequence at positions 1475-1514 (SEQ ID NO: 49), the amino acid sequence at positions 1515-1719 (SEQ ID NO: 50), the amino acid sequence at positions 1764-1944 (SEQ ID NO: 51) and the amino acid sequence at positions 2096-2529 (SEQ ID NO: 52) of the cadherin EGF LAG seven-pass G-type receptor 3,

<32> (j) the amino acid sequence at positions 54-159 (SEQ ID NO: 53), the amino acid sequence at positions 160-268 (SEQ ID NO: 54), the amino acid sequence at positions 269-383 (SEQ ID NO: 55), the amino acid sequence at positions 384-486

(SEQ ID NO: 56) and the amino acid sequence at positions 487-612 (SEQ ID NO: 57) of an osteoblast specific cadherin (OB-cadherin).

<33> The N-terminal end of the peptide has an addition of cysteine and two glycines so as to stabilize the structure of the peptide and to facilitate chemical immobilization of the peptide to the barrier membrane.

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<35> As the barrier membrane to be surface-activated by the present invention, all kinds and types of barrier membranes can be used if they are used in the technical field. Pre Preferred examples of these barrier membranes include porous membranes made of polylactic acid, regeneraton membranes made of nanofibers of chitin or chitosan, and film-shaped barrier membranes made of chitin or chitosan. Also, as the implants, titanium implants are preferably used but are not limited thereto. In this respect, the surface of the implants is preferably modified by oxidation and nitrification so as to facilitate the adhesion of the active peptide to the surface.

VERIFICATION OF TRANSLATION

I, BAE, Young Sim of 11th Yeosam Bldg., 648-23, Yeoksam-dong, Gangnam-gu, Seoul, 135-080, Republic of Korea

State that the attached document is a true and accurate translation of Korean Patent Application No. 10-2004-0019010 in Korean (language of original specification) to the best of my knowledge and belief.

Dated this August 3, 2009

Signature of Translator: